

Access DB#

70504

**SEARCH REQUEST FORM**

Scientific and Technical Information Center

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**If more than one search is submitted, please prioritize searches in order of need.**

\*\*\*\*\*

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc. if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: \_\_\_\_\_

Inventors (please provide full names): \_\_\_\_\_

Earliest Priority Filing Date: \_\_\_\_\_

*\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Jan Delaval  
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Searcher: <u>Jan</u>	NA Sequence (#) <input checked="" type="checkbox"/>	STN _____
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Online Time: <u>10</u>	Other _____	Other (specify) _____

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the 1990s, the number of people in the UK who are aged 65 and over has increased from 10.5 million to 12.5 million, and the number of people aged 75 and over has increased from 4.5 million to 6.5 million (Office of National Statistics 2000). The number of people aged 65 and over is projected to increase to 15.5 million by 2020, and the number of people aged 75 and over to 8.5 million (Office of National Statistics 2000). The increase in the number of people aged 65 and over is due to a combination of factors, including a decline in the birth rate, a decline in the death rate, and a decline in the rate of emigration.

The increase in the number of people aged 65 and over has led to a corresponding increase in the number of people who are dependent on others for their care. In 1990, there were 1.5 million people aged 65 and over who were dependent on others for their care, and this number is projected to increase to 2.5 million by 2020 (Office of National Statistics 2000). The increase in the number of people who are dependent on others for their care is due to a combination of factors, including a decline in the birth rate, a decline in the death rate, and a decline in the rate of emigration.

The increase in the number of people who are dependent on others for their care has led to a corresponding increase in the number of people who are living in care homes. In 1990, there were 1.5 million people aged 65 and over who were living in care homes, and this number is projected to increase to 2.5 million by 2020 (Office of National Statistics 2000). The increase in the number of people who are living in care homes is due to a combination of factors, including a decline in the birth rate, a decline in the death rate, and a decline in the rate of emigration.

The increase in the number of people who are living in care homes has led to a corresponding increase in the number of people who are living in care homes who are dependent on others for their care. In 1990, there were 1.5 million people aged 65 and over who were living in care homes who were dependent on others for their care, and this number is projected to increase to 2.5 million by 2020 (Office of National Statistics 2000). The increase in the number of people who are living in care homes who are dependent on others for their care is due to a combination of factors, including a decline in the birth rate, a decline in the death rate, and a decline in the rate of emigration.

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Location/Qualifiers				

[illegible][illegible]

1. The first group of variables includes the demographic characteristics of the respondents, such as age, gender, and education level. These variables are used to control for potential confounding factors that may influence the relationship between the independent and dependent variables.

Journal (988802), 988906, 1(98881

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7. *Notes* 1992

Figure 1. Schematic representation of the experimental design. The subjects were divided into two groups: the control group (CG) and the experimental group (EG). The CG was divided into two subgroups: the control group (CG) and the control group (CG). The EG was divided into two subgroups: the experimental group (EG) and the experimental group (EG). The subjects were divided into two groups: the control group (CG) and the experimental group (EG). The CG was divided into two subgroups: the control group (CG) and the control group (CG). The EG was divided into two subgroups: the experimental group (EG) and the experimental group (EG).

**NOVEL NITROGEN**

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**REGISTRATION OF THE COMPANY**

ΔΙΕΥΘΥΝΤΗΣ: Μ.Λ. ΒΕΛΩΝΙΔΗΣ

OSU-ADP-HIT-PO-PAV-YIAI

# Abstract

NISAKUICHI FUDAIJOKI

VIAGUAI,AIMI,AKNVMI,JIJI,OTI,JI,PI

$$1984(1)7, 1(1)8, 88(1)6,$$

**Figure 1**

"211N" 11.15/

108918-109509

Number 2

40102 "No. 2"

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**A**

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100







pass sequencing reads from expressed RNA complementary aligned to the genomic DNA sequence from the bacterial clone (3746, GAB69725).

The EST sequences listed match this sequence with an identity of at least 95% between the coordinates shown.

Further information can be found at

http://www.ncbi.nlm.nih.gov/ESTBLAST/blast/seq/blast.cgi?seq=us-09-816-697-1

# FEATURES

source

1..1600

Organization "Homo sapiens"

GB accession "209"

Genome "209"

1..350

Feature "Matches EST AF047464 from clone IMAGC1866464"

1..89

Feature "Matches EST AF047464 from clone IMAGC1866464"

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misc\_feature complement (1412..1600)

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Feature "Matches EST AF047464 from clone IMAGC1866464"

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Feature "Matches EST AF047464 from clone IMAGC1866464"

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Feature "Matches EST AF047464 from clone IMAGC1866464"















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1. (1997)

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/feature "Homo sapiens"







JOURNAL  
 COMMENT  
 Contact: Robert Strausberg, Ph.D.  
 Email: rcp@broad.mit.edu  
 This clone is available royalty-free through EMBL. To contact the  
 IMAGE Consortium (info: image@imgl.mcgill.ca) for further information,  
 insert keyword: 818 Std Error: 0.00  
 Seq primer: -400p from Gibco  
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 /clone "IMAGE:1847195"  
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 /lab\_host "DH10"  
 /note "Tumor tissue, Vector: pTZ19-Pac (Pharmacia) with  
 a modified polylinker Site 1. Not in Site 2. Eco RI:  
 equal amounts of plasmid DNA from three normalized  
 libraries (total lung NBH119W, testis NHT, and B cell  
 N1-30A1-3CH1) were mixed, and ss clones were made in  
 vitro. Following HAP purification, this DNA was used as  
 tracer in a subtractive hybridization experiment. The driver  
 was PCR amplified cDNAs from pools of 5,000 clones made  
 from the same 3 libraries. The pools consist of:  
 1. M.A.G.E. clones 297480-402087, 682632-687239,  
 726408-728711, and 729096-731999. Subtraction by Benzo  
 Sources and M. Patricia Bonaldi.  
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 query Match 48.4% Score 460 Db % Length 460  
 Best local Similarity 100.0% Freq No. % 67  
 Matches 460: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

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 Homo sapiens  
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 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 REFERENCE  
 1. (bases 1 to 460)  
 de la Cruz, J., et al., 1999, J. Neurosci.  
 TITLE  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP)  
 Tumor gene index  
 JOURNAL  
 COMMENT  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: rcp@broad.mit.edu  
 This clone is available royalty-free through EMBL. To contact the  
 IMAGE Consortium (info: image@imgl.mcgill.ca) for further information,  
 possible reversed clones, poly not found  
 Seq primer: -400p from Gibco  
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 N1-30A1-3CH1) were mixed, and ss clones were made in  
 vitro. Following HAP purification, this DNA was used as  
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 was PCR amplified cDNAs from pools of 5,000 clones made  
 from the same 3 libraries. The pools consist of:  
 1. M.A.G.E. clones 297480-402087, 682632-687239,  
 726408-728711, and 729096-731999. Subtraction by Benzo  
 Sources and M. Patricia Bonaldi.  
 BASE COUNT  
 origin 87 a 145 c 146 g 92 t  
 query Match 48.4% Score 460 Db % Length 460  
 Best local Similarity 100.0% Freq No. % 67  
 Matches 460: Conservative 0: Mismatches 0: Indels 0: Gaps 0:



| Ch | Ref | Accession | Gene     | Strain | Length | Start | Stop | Strand | Quality                           |
|----|-----|-----------|----------|--------|--------|-------|------|--------|-----------------------------------|
| 24 | 459 | AA040706  | AM459821 | Human  | 400    | 1     | 400  | +      | High quality sequence, stop: 108. |
| 25 | 254 | U04440    | hsp70    | Human  | 415    | 1     | 415  | +      |                                   |
| 26 | 459 | U04440    | hsp70    | Human  | 415    | 1     | 415  | +      |                                   |
| 27 | 459 | U04440    | hsp70    | Human  | 415    | 1     | 415  | +      |                                   |
| 28 | 459 | U04440    | hsp70    | Human  | 415    | 1     | 415  | +      |                                   |
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| ORIGIN      | 726408-726711, and 726096-721359, Subtraction by Institute<br>Saares and M. Fatima Roldado, " |       |       |      |  |

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| /"stone"     | "MAGE:2090121"         |
| /"stone:110" | "Sources:NEI_T_110_11" |



miRNA sequencing

Version: 81409523.1 01:15170446

**KELWORTH  
EST.  
SOUTH HOUSE**

## DISCUSSION

REHERN, I (b. 1907) 742.















[illegible][illegible]















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11 07-SEP-2000; 200000S-0216680.
12 11-SEP-2000; 200000S-0217447.
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14 11-SEP-2000; 200000S-0218299.
15 26-SEP-2000; 200000S-0220063.
16 26-SEP-2000; 200000S-0220094.
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18 14-AUG-2000; 200000S-0224519.
19 14-AUG-2000; 200000S-0225214.
20 14-AUG-2000; 200000S-0225214.
21 14-AUG-2000; 200000S-0225266.
22 14-AUG-2000; 200000S-0225267.
23 14-AUG-2000; 200000S-0225270.
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| DH                    | 404   | CGTCCTCATACTGGCTCATCTGGAGCTGGCTGCTGGCTGGCTGGCTGGCTGGCT      | 468   |
| DY                    | 642   | GTTGGGAGGCTGCTGGGCTGCTGGGCTGCTGGGCTGCTGGGCTGCTGGGCTGCTGGGCT | 698   |
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| AC                    |   |   |       |
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| XX                    |   |   |       |
| DE                    | HSV-2 strain SH5 (contig ID 11 DNA sequence).                             |   |       |
| XX                    |   |   |       |
| KM                    | HSV-2 strain SH5: immunological response induction therapy;               |   |       |
| KM                    | and viral identification; viral protein inhibition; ss.                   |   |       |
| XX                    |   |   |       |
| GC                    | Report of type 2.   |   |       |
| FH                    | Roy   | Location/Qualifiers   |       |
| FI                    | CHS   | Completion (1..2441)  |       |
| FI                    |   | /start at   |       |
| FI                    |   | protein receptor (page 1, at AAT AAA AAA AAA)               |       |
| FI                    |   | protein car transporter amino acid transport carrier        |       |
| FN                    | W90820016-A1.   |   |       |
| FD                    | 14 MAY-1998.  |   |       |
| XX                    |   |   |       |
| FE                    | 61 OCT-1997   | 97WC-US20016.   |       |
| XX                    |   |   |       |
| FX                    | 09 JUN-1997   | 97US-0049018.   |       |
| FX                    | 04 NOV-1996   | 96NS-0239279.   |       |
| FA                    | (SMK ) SMITHLINE BEECHAM CORP.  |   |       |
| XX                    |   |   |       |
| FI                    | Chen JY, Dabrowski-Amaraal CB, Deleventro AM, Dillon SB,                  |   |       |
| FI                    | Besser KM, Leary JJ   |   |       |
| XX                    |   |   |       |
| OR                    | W91: 1998-286847/25.  |   |       |
| DR                    | P-1258; AAV6.2104.  |   |       |
| XX                    |   |   |       |
| FI                    | Biogenesis virus type 2 sequences used in v.c. prevent ion                |   |       |
| FI                    | and treatment of infection or induction immunological response in         |   |       |
| FI                    | mammal  |   |       |
| XX                    |   |   |       |
| PS                    | claim 1; page 400; 748pp; English.  |   |       |
| XX                    |   |   |       |
| XX                    | This sequence represents a herpes simplex virus type 2 (HSV-2) RNA        |   |       |
| CC                    | sequence of the invention. This sequence was isolated from HSV-2 strain   |   |       |
| CC                    | SH5 (deposited as ATCC VR-246), is designated contig ID 11, and encodes   |   |       |
| CC                    | a HSV-2 protein. The protein can be used for the treatment or             |   |       |
| CC                    | prevention of disease, to induce an immunological response in a mammal or |   |       |
| CC                    | to identify inhibitors, activators or novel antivirals. Antagonists of    |   |       |
| CC                    | the proteins can be used to inhibit a viral polypeptide. The DNA sequence |   |       |
| CC                    | of a vector containing it can also be used to induce an immunological     |   |       |
| CC                    | response in a mammal.   |   |       |
| XX                    |   |   |       |
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| <hr/>                 |   |   |       |
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| Best Local Similarity | 49.6%, Pval.No.: 0.000352   |   |       |



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NUMBER OF SEQUENCES: 76  
CORRESPONDING ADDRESS:  
ADDRESSER: BIRCH, STEWART, KOLASCH & BIRCH

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1  APPLICANT:  Lewis, Randolph V.
2  AEEICANT:  Colquhoun, Mark
3  TITLE OF INVENTION:  Straps Encircling Minor Amputated Spider

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1  SOFTWARE: Patent in boldface #1.0, Version #1.30
2  CURRENT APPLICATION DATA:
3  APPLICATION NUMBER: 05/597,491
4  FILING DATE:
5  CLASSIFICATION:
6  PRIOR APPLICATION DATA:
7  APPLICATION NUMBER: US 08/901,200
8  FILING DATE: 28 JUL 1997
9  ATTORNEY/AGENT: McFARLANE
10 NAME: METTERS, THOMAS C.
11 REGISTRATION NUMBER: 46,969
12 REFERENCE/EXCISE NUMBER: 787-0761V2
13 TELECOMMUNICATION INFORMATION:
14 TELEPHONE: (508) 445-9001
15 TELEFAX: (508) 445-6951
16 INFORMATION FOR USE TO NC: 11:
17 SEQUENCE CHARACTERISTICS:
18 LENGTH: 884 base pairs
19 TYPE: nucleic acid
20 STRANDEDNESS: single
21 TOPOLOGY: linear
22 MOLECULE TYPE: DNA (genomic)
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25 LOCATION: 1..884
26 OTHER INFORMATION: /note="bold & genomic sequence"
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30 OTHER INFORMATION: /note="EXON ONE"
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35 OTHER INFORMATION: FEATURES 884 IN THIS SEQUENCE AND
36 POSITION 1 IN CING TO NO. 14"
37 US 08 219 491 11

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GenTools version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd

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(without alignment)

1741. 0688 Million cell updates/sec

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Section in table: HLFSIM6,2

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`library(10.0) , library(0.5)`

Searched: 28113 seqs, 9608934 residues

Total number of hits satisfying chosen parameters: 268148

Minimum TOR seq length: 0

Maximum IR seq length: 2000000000

Post-Processing: Minimum Not Chosen

Maximum Match 100%

Listing first 45 summaries

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1:  pir1:*
2:  pir2:*
3:  pir3:*
4:  pir4:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

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| 1          | 117   | 7.1         | 952    | 2  | E94534 | hypothetical protein                       |
| 2          | 116   | 7.0         | 1010   | 2  | A14977 | hypothetical structural protein            |
| 3          | 111   | 6.7         | 473    | 2  | F50420 | non-erythroid alpha globin                 |
| 4          | 111   | 6.7         | 1104   | 3  | F49745 | erythroid alpha globin                     |
| 5          | 111   | 6.7         | 2472   | 1  | S16HHA | Spectrin, alpha chain                      |
| 6          | 102.5 | 6.2         | 1137   | 1  | S17445 | gamma 1 spectrin                           |
| 7          | 102   | 6.2         | 1030   | 2  | A12612 | Spectrin, alpha chain                      |
| 8          | 101   | 6.1         | 1425   | 1  | S17560 | beta 1 spectrin                            |
| 9          | 99.5  | 6.0         | 705    | 2  | A45363 | synapsin I splice variant                  |
| 10         | 99    | 6.0         | 478    | 2  | A37671 | synapsin I                                 |
| 11         | 99    | 6.0         | 2472   | 2  | A35915 | footin alpha chain                         |
| 12         | 98    | 5.9         | 456    | 2  | F31609 | footin alpha chain                         |
| 13         | 97.5  | 5.9         | 420    | 2  | T08691 | hypothetical protein                       |
| 14         | 97    | 5.9         | 4684   | 2  | A59404 | hypothetical protein                       |
| 15         | 96    | 5.8         | 441    | 2  | C83418 | placental importin                         |
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| 23         | 93    | 5.6         | 401    | 2  | I49046 | hypothetical protein                       |
| 24         | 93    | 5.6         | 475    | 2  | B27671 | Spectrin, alpha chain                      |
| 25         | 93    | 5.6         | 1366   | 2  | I35905 | probable major protein                     |
| 26         | 92.5  | 5.6         | 814    | 2  | T05677 | probable serine/threonine kinase           |
| 27         | 92    | 5.6         | 305    | 2  | F13916 | probable serine/threonine kinase           |
| 28         | 92    | 5.6         | 706    | 2  | E30411 | synapsin II, low molecular weight protein  |
| 29         | 92    | 5.6         | 1033   | 2  | F42761 | synapsin II, high molecular weight protein |

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| 31 | 91   | 5.5 | 438  | 2 | D75197 | tRNA-met-leu-1           |
| 42 | 91   | 5.5 | 640  | 2 | S67656 | hypothetical protein     |
| 43 | 91   | 5.5 | 892  | 2 | T24420 | probable transferase     |
| 44 | 90.5 | 5.5 | 143  | 2 | I40731 | probable acylase         |
| 45 | 90.5 | 5.5 | 292  | 2 | H72670 | hypothetical protein     |
| 46 | 90.5 | 5.5 | 472  | 2 | D75708 | probable protein         |
| 47 | 90.5 | 5.5 | 543  | 2 | F76583 | cellulose family protein |
| 48 | 90   | 5.5 | 545  | 2 | B70374 | conserved hypothetical   |
| 49 | 90   | 5.5 | 1446 | 1 | A45644 | conservative glycolytic  |
| 40 | 90   | 5.5 | 1440 | 1 | EDHEP  | immunosorbent polymer    |
| 41 | 89.5 | 5.4 | 435  | 2 | S18512 | proteinase               |
| 42 | 89   | 5.4 | 1162 | 2 | D84854 | conserved hypothetical   |
| 43 | 89   | 5.4 | 4687 | 1 | A39638 | protein                  |
| 44 | 88.5 | 5.4 | 950  | 2 | F86286 | hypothetical protein     |
| 45 | 88.5 | 5.4 | 2591 | 2 | I40288 | protein                  |

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Resubmitted to the EMBL Data Library, September 1999

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QY 97 ---QVIVT---QVSHNNAVLEF KSTFAALQKAL 127
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QY 161 LQFYGLHVAIRGVRSK-----PELD-----PLTRPELR EAPATRAVAY 202
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Db 248 FVGLTFAH FVGLTFAH FVGLTFAH FVGLTFAH FVGLTFAH 304
QY 203 RALELLIRVLDKELTARPAAPALCAVILGIRDLRPAFAVAHPKALRLQARSG 262
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Db 302 PAIGVCT SAMPVPEPLQSPEDHVAAGAVIYVAFKRSAAVYSAFNANPQVANSKRE 360
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 Job Time: 151 Sec



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| DR | HSPG:  | P17599;    | LAXX.        |   |
| DR | MM:  | K13440;    | -            |   |
| DR | InterPro:  | IPR001359; | Synapsin     |   |
| DR | ProDom:  | PRO2378;   | Synapsin_2.1 |   |
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| DR | ProSITE:   | PS00415;   | SYNAPSIN     |   |
| DR | ProSITE:   | PS00416;   | SYNAPSIN     |   |
| KW | Synapse; Phosphorylation; Neurone; Repeat; Actin binding;<br>Alternative splicing. |            |              |   |
| FT | DOMAIN   | 1          | 28           | A.  |
| FT | DOMAIN   | 29         | 112          | B (LINKER).   |
| FT | DOMAIN   | 113        | 420          | C. ACTIN BINDING AND CYTOSKELETAL<br>BINDING.   |
| FT | DOMAIN   | 421        | 655          | D (PRO-RICH LINKER).  |
| FT | DOMAIN   | 656        | 705          | E.  |
| FT | MOD_RES  | 9          | 9            | PHOSPHORYLATION (BY CKAP AND<br>CAM KINASE I)   |
| FT | MOD_RES  | 568        | 568          | PHOSPHORYLATION (BY CAM KINASE II).   |
| FT | MOD_RES  | 605        | 605          | PHOSPHORYLATION (BY CAM KINASE III).  |
| FT | VARIABLE   | 647        | 647          | GLUTAMATE ACETYLATION (BY<br>G-3.5.1.3A). ACETYLATION (BY<br>MISSING (IN SYNAPSIN IB)).<br>G -> E (IN MP. 3). |
| FT | VARIABLE   | 670        | 705          |   |
| FT | CONFLICT   | 148        | 148          |   |
| SC | SEQUENCE   | 705 AA.    | 73954 MW.    | 40783112475062177014.   |

[illegible]

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| RESULT | 8  |
| ID     | SRRX_HUMAN   |
| AC     | SDY5W9; 694885;  |
| D7     | 16 OCT 2001 (Rel. 40), Created)  |
| D7     | 16 OCT 2001 (Rel. 40), Last sequence update)                               |
| D7     | 16-OCT-2001 (Rel. 40), Last annotation update)                             |
| D7     | Sorting nexin 11.  |
| DE     | SNX11.   |
| DN     |  |
| OS     | Homo sapiens (Human).  |
| OC     | Eukaryota; Metazoa; Chordata; Mammalia; Artiodactyla; Eutrypastroni;       |
| OC     | Mammalia; Eutheria; Primates; Carnivora; Homiidae; Homo.                   |
| OX     | NCBI_Taxid: 9606;  |
| RN     | [1]  |
| RA     | SEQUENCE FROM N.A.   |
| RA     | Toasdale R.D., Giverson P.A., Karlsson L.;                                 |
| RT     | "Identification of eleven novel human sorting nexin molecules. A sub-      |
| RT     | group of the sorting nexin family is associated with the early             |
| RT     | endosomes."  |
| RI     | Endocrinology 147(1997) 111-120, 1997, pubmed, pmid: 9174059.              |
| RN     | [2]  |
| RP     | SEQUENCE FROM N.A.   |
| KC     | Tissue=Thyroid;  |
| RA     | Ishida T., Ota T., Hayashi K., Saitoh Y., Ito S., Suzuki Y.,               |
| RA     | Nishikawa T., Naito Y., Sakurai F., Yoshida-Horiuchi A., Hara H.,          |
| EA     | Laiuso T., Nemura Y., Nakamura Y., Kimura K., Takemachi K.,                |
| EA     | Arita M., Hatakeyama S., Ishii K., Kawai Y., Saito K., Yamamoto J.,        |
| KA     | Wakamatsu A., Nakamura Y., Nakahara K., Masuda Y., Yoshida A.;             |
| KT     | "Retroviral gene expression by two-dimensional electrophoresis"            |
| RN     | [3]  |
| RP     | SEQUENCE FROM N.A.   |
| KC     | Tissue=Kidney;   |
| RA     | Strausberg R.;   |
| RA     | Strausberg R.V. et al. The proteomic database.                             |
| CC     | -1- EDUCATION MAY BE INVOLVED IN SEVERAL STAGES OF INTRACELLULAR           |
| CC     | TRAFFICKING.   |
| CC     | -1- SIMILARITY: BELONGS TO THE SORTING NEXIN FAMILY.                       |
| CC     | -1- SIMILARITY: CONTAINS 1 PROX HOMOLOG (PX) DOMAIN.                       |
| CC     | -1- CATION: IT IS UNCERTAIN WHETHER MET 1 OR MET 7 IS THE INITIATOR.       |
| CC     |  |
| CC     | This Swiss Prot entry is copyright. It is produced through a collaboration |
| CC     | between the Swiss Institute of Bioinformatics and the EMBL consortium.     |
| CC     | The European Bioinformatics Institute. There are no restrictions on its    |
| CC     | use by non-profit institutions as long as its content is in no way dis-    |
| CC     | modified and thus statement is not removed, reused and/or commercialized   |
| CC     | or sold on email to license agreement. See http://www.ebi.ac.uk/copyright/ |
| DR     | EMBL; AF121861; AA027844.1; ALT_INIT.                                      |
| DR     | EMBL; AK925942; FA034742.1;  |
| DR     | EMBL; BC000768; AAH00768.1;  |
| DR     | Fairclough D.; IP001684; PX.   |
| DR     | Pfam; PF00787; PX; 1.  |
| DR     | SMART; SM0312; PX; 1.  |
| FT     | Transport: Protein transport.  |
| FT     | CNAME 21   |
| SEQ    | SEQUENCE 270 AA: 30433 MW: 6683987415F1724F CRC64:                         |

Query Match: 5, 99; Score: 97; DB: 1; Length: 270;  
 Best Local Similarity: 22.0%; Prot. No. 0.52;  
 Matches: 59; Conservation: 11; Mismatches: 96; Gaps: 72; Gaps: 144

[illegible][illegible]





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01 SYSTEM RESPONSIBLE FOR THE OXIDATIVE FIRST IN WHICH ELECTRON ARE
02 TRANSFERRED FROM NADPH TO NADPH+2. WHEN THE ELECTRON ARE TRANS-
03 FERRED FROM NADPH TO NADPH+2, THE ELECTRON ARE TRANSFERRED FROM
04 NADPH TO NADPH+2. THE ELECTRON ARE TRANSFERRED FROM NADPH TO
05 NADPH+2. THE ELECTRON ARE TRANSFERRED FROM NADPH TO NADPH+2.
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61 AUG-1996 (loc. 15, created)  
 62 01 FEB-1996 (loc. 33, last sequence update)  
 63 01 MAY-2000 (loc. 39, last annotation update)  
 64 Synapsin 1.  
 65  
 66 008 Taurus (bovine).  
 67 Fukuyama, Motoyasu, Choudhary, Grammat, Vortelak, Polychronis;  
 68 Mammalian Brain: Localization of Synapsin 1; Journal of Neurocytochemistry; 1997; 46: 103-112.  
 69  
 70 009 Bovine (bovine).  
 71 Nishi, Takashi; 1991;  
 72 111  
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 74 SEQUENCE FROM N.A.  
 75 TISSUE: Brain;  
 76 METHOD: cDNA; 2506642;  
 77 Smith, L.C., Greenberg, A.J., Ko, H.-P., Lavee, Y., Robinson, P.A.,  
 78 Bickford, A., Kanaoui, S.D., Walter, M.A., Portin, M.S., de Camilli, P.,  
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 80 "Synapsin: associates of shroud and individual domains in a family of  
 81 proteins involved in synaptic transmission."  
 82 Science 245:1474-1480(1989).  
 83 121  
 84 THE SUBSTRATE SITE FOR PROLINE DIRECTION KINASE.  
 85 MEDLINE 92314728; PubMed 2108663;  
 86 Ball, F., Mitchell, J.P., Walling, P.R.;  
 87 "Phosphorylation of synapsin I at a novel site by proline directed  
 88 protein kinase."  
 89 J. Biol. Chem. 265:6944-6948(1990).  
 90 141  
 91 X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS) OF 112-417.  
 92 MEDLINE 98160589; PubMed 9653375;  
 93 Sessio, L., Wang, C.R., Hosaka, M., Shoguchi, S., Suedhof, T.C.,  
 94 Robinson, L.;  
 95 "Synapsin I is structurally similar to ATP-utilizing enzymes."  
 96 J. Biol. Chem. 267:12771-12780(1992).  
 97 1 FUNCTION: PROTEIN, PHOSPHOPROTEIN THAT CATALYZES SYNAPTIC VESICLE,  
 98 KININS TO THE CYTOSKELETON, AND IS BELIEVED TO FUNCTION IN THE  
 99 REGULATION OF NEUROTRANSMITTER RELEASE.  
 100 2 SUBCELLULAR LOCATION: SYNAPTIC;  
 101 3 ALTERNATIVE PRODUCTS: 2 isoforms, SYNAPSIN 1A (GENE NAME) AND  
 102 SYNAPSIN 1B, ARE DESCRIBED BY ALTERNATIVE SPLICING.  
 103 4 FURTHER INFORMATION: AT LEAST FIVE DIFFERENT PROTEIN KINASES, IT IS  
 104 PROBABLE THAT PHOSPHORYLATION PLAYS A ROLE IN THE REGULATION OF  
 105 SYNAPSIN 1 IN THE NERVE TERMINAL.  
 106 5 SIMILARITY: BELONGS TO THE SYNAPSIN FAMILY.  
 107  
 108 THIS SWISS PROTEIN ENTRY IS COPYRIGHTED. IT IS PRODUCED THROUGH A COLLABORATION  
 109 BETWEEN THE SWISS INSTITUTE OF BIOETHICS AND THE EMBL INSTITUTION.  
 110 THE EUROPEAN BIOINFORMATICS INSTITUTE, THERE ARE NO RESTRICTIONS ON ITS  
 111 USE BY ANY OTHER INSTITUTION AS LONG AS ITS CONTENT IS IN NO WAY  
 112 MODIFIED AND THIS STATEMENT IS NOT REMOVED, MISUSE BY AND FOR COMMERCIAL  
 113 PURPOSES IS EXPRESSLY PROHIBITED. HELP OF SWISS INSTITUTE OF BIOETHICS  
 114 OR SEND AN EMAIL TO: EMBL@SWISS-ETH.CH.  
 115  
 116 EMBL: M278107; AAA00761.1;  
 117 EMBL: M27811; AAA00762.1;  
 118 EMBL: A15758; A15758;  
 119 EMBL: E30411; E30411;  
 120 EMBL: F30411; F30411;  
 121 EMBL: J409; J409;  
 122 EMBL: J409; J409;  
 123 EMBL: J409; J409;  
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-M protein - protein search, using sw model

Run on: July 9, 2002, 15:46:40 : Search time 30.14 seconds

(without alignments)  
1813.747 Million cell updates/sec

Filter:  
Percent scores: 95-09-816-697-2

Sequences: 1 MASPHEROSMA.MHI001.....KREIPIKIKREIPIKREIPIK...M

Scoring table:  
R100S006Z

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994229 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: SP|KMBL\_1%\*  
2: SP|actin:\*  
3: SP|fibrin:\*  
4: SP|human:\*  
5: SP|invertebrate:\*  
6: SP|mammal:\*  
7: SP|mus:\*  
8: SP|ornanella:\*  
9: SP|phage:\*  
10: SP|plant:\*  
11: SP|rodent:\*  
12: SP|virus:\*  
13: SP|vertebrate:\*  
14: SP|unclassified:\*  
15: SP|FVIRUS:\*  
16: SP|bacteriophage:\*  
17: SP|archaeo:\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score  | Query Match | Length | DB ID | Accession |
|------------|--------|-------------|--------|-------|-----------|
| 1          | 1253.5 | 76.0        | 313    | 11    | Q9D2Y5    |
| 2          | 419    | 25.4        | 372    | 4     | Q9HR16    |
| 3          | 413.5  | 25.1        | 373    | 4     | Q969T3    |
| 4          | 210    | 12.7        | 326    | 5     | Q9ERT6    |
| 5          | 185.5  | 11.2        | 295    | 5     | Q9W0C1    |
| 6          | 122    | 7.4         | 162    | 4     | Q14612    |
| 7          | 122    | 7.4         | 169    | 11    | Q9W0C1    |
| 8          | 118    | 7.2         | 169    | 4     | Q9W0C1    |
| 9          | 117    | 7.1         | 192    | 10    | Q9W0C1    |
| 10         | 116    | 7.0         | 1910   | 3     | Q90SNI    |
| 11         | 115.5  | 7.0         | 450    | 5     | Q9SKR3    |
| 12         | 114.5  | 6.9         | 431    | 5     | Q9K4B9    |
| 13         | 113    | 6.8         | 169    | 11    | Q9W0C1    |
| 14         | 112.5  | 6.8         | 435    | 4     | Q96192    |
| 15         | 111    | 6.7         | 473    | 13    | Q90990    |
| 16         | 110.5  | 6.7         | 577    | 10    | Q941X3    |

|    |       |     |      |    |        |                    |
|----|-------|-----|------|----|--------|--------------------|
| 17 | 109.5 | 6.6 | 582  | 11 | Q91WB6 | Q91WB6 mus muscula |
| 18 | 107   | 6.5 | 520  | 5  | Q9VKR1 | Q9VKR1 drosophila  |
| 19 | 103.5 | 6.3 | 387  | 4  | Q96FW4 | Q96FW4 homo sapien |
| 20 | 101.5 | 6.2 | 450  | 11 | Q91YJ2 | Q91YJ2 mus muscula |
| 21 | 101   | 6.1 | 1325 | 4  | Q90G16 | Q90G16 homo sapien |
| 22 | 100.5 | 6.1 | 450  | 4  | Q96C71 | Q96C71 homo sapien |
| 23 | 99.5  | 6.0 | 515  | 4  | Q96R07 | Q96R07 homo sapien |
| 24 | 99.5  | 6.0 | 549  | 4  | Q9NXP8 | Q9NXP8 homo sapien |
| 25 | 99.5  | 6.0 | 1065 | 10 | Q91WZ8 | Q91WZ8 ratu        |
| 26 | 99    | 6.0 | 475  | 11 | Q93463 | Q93463 ratu        |
| 27 | 99    | 6.0 | 1041 | 10 | Q9AS44 | Q9AS44 oryza sativ |
| 28 | 98.5  | 6.0 | 204  | 4  | Q96194 | Q96194 homo sapien |
| 29 | 98.5  | 6.0 | 722  | 4  | Q9BOM1 | Q9BOM1 homo sapien |
| 30 | 98.5  | 6.0 | 1764 | 5  | Q9N908 | Q9N908 testis      |
| 31 | 98    | 5.9 | 461  | 5  | Q90277 | Q90277 drosophila  |
| 32 | 98    | 5.9 | 565  | 5  | Q9R373 | Q9R373 drosophila  |
| 33 | 98    | 5.9 | 654  | 11 | Q90T05 | Q90T05 mus muscula |
| 34 | 97.5  | 5.9 | 476  | 11 | Q9D483 | Q9D483 mus muscula |
| 35 | 97.5  | 5.9 | 491  | 5  | Q9V794 | Q9V794 drosophila  |
| 36 | 97.5  | 5.9 | 1295 | 10 | Q9FNB3 | Q9FNB3 arabidopsi  |
| 37 | 97    | 5.9 | 395  | 11 | Q9CCE0 | Q9CCE0 mus muscula |
| 38 | 97    | 5.9 | 595  | 11 | Q91WB2 | Q91WB2 mus muscula |
| 39 | 97    | 5.9 | 1015 | 10 | Q941J2 | Q941J2 oryza sativ |
| 40 | 97    | 5.9 | 1030 | 10 | Q9A8S4 | Q9A8S4 oryza sativ |
| 41 | 96    | 5.8 | 441  | 16 | Q910M5 | Q910M5 pseudomus   |
| 42 | 96    | 5.8 | 595  | 4  | Q9HS17 | Q9HS17 homo sapien |
| 43 | 96    | 5.8 | 1038 | 10 | Q94C83 | Q94C83 oryza sativ |
| 44 | 95.5  | 5.8 | 373  | 16 | Q9PA13 | Q9PA13 xyelia fus  |
| 45 | 95.5  | 5.8 | 498  | 16 | P73091 | P73091 synechocyst |

## ALIGNMENTS

| RESULT | ID  | PRELIMINARY | PRT | 313 AA |
|--------|---|-------------|-----|--------|
| Q9D2Y5 | Q9D2Y5  |             |     |        |
| AC     | Q9D2Y5  |             |     |        |
| DI     | 01-JUN-2001 (TREMBLrel. 17, Created)                                  |             |     |        |
| DT     | 01-JUN-2001 (TREMBLrel. 17, last sequence update)                     |             |     |        |
| DE     | 01-DEC-2001 (TREMBLrel. 19, last annotation update)                   |             |     |        |
| DE     | Q130017C17R1K PROTEIN (SNX20).  |             |     |        |
| GN     | Q130017C17R1K OR SNX20.   |             |     |        |
| OS     | Mus musculus (Mouse).   |             |     |        |
| OC     | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;               |             |     |        |
| OC     | Mammalia; Eutheria; Rodentia; Sciurimorphi; Muridae; Murinae; Mus;    |             |     |        |
| OX     | NCBI_TaxID=10090;   |             |     |        |
| RN     |   |             |     |        |
| RF     | SEQUENCE FROM N.A.  |             |     |        |
| RC     | STRATN 55786/601; PROSD GROM;   |             |     |        |
| RX     | REPLIND:21085660; PubMed:11217851;                                    |             |     |        |
| RA     | Kawati J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,   |             |     |        |
| RA     | Arakawa T., Imai A., Fujimichi Y., Kono H., Abechi T., Furuta S.,     |             |     |        |
| RA     | Aizawa K., Ikazaki M., Nishi K., Kiyosaka H., Fudo S., Yamada I.,     |             |     |        |
| RA     | Saito T., Ikazaki Y., Kobayashi I., Hono H., Kasekawa T., Saito K.,   |             |     |        |
| RA     | Kadota K., Matsuda H.A., Ashihara M., Naitoh S., Kasai H.,            |             |     |        |
| RA     | Fleischmann W., Gaasterland T., Gissi C., Kim H., Kothaka H.,         |             |     |        |
| RA     | Kuehl P., Lewis S., Matsuo Y., Nakano T., Pesole G., Quackenbush J.,  |             |     |        |
| RA     | Schriml L.M., Staubli F., Suzuki R., Tomita M., Wadner L., Washio T., |             |     |        |
| RA     | Sakai K., Okada T., Furuno M., Aono H., Baldarelli R., Barish G.,     |             |     |        |
| RA     | Blake J., Battelli D., Bojano N., Carlini P., de Bonaldi M.,          |             |     |        |
| RA     | Brownstein M.J., Butt G., Fletcher C., Fujita M., Gariboldi M.,       |             |     |        |
| RA     | Gustinchin S., Hill D., Hofmann M., Hone U.A., Kanlaya M., Lee N.H.,  |             |     |        |
| RA     | Lyden P., Marchionni L., Marzetta A., Mazzanti J., Montanari P.,      |             |     |        |
| RA     | Radovic T., Rana B., Riboldi M., Roldanov L., Sakamoto R.,            |             |     |        |
| RA     | Sakai H., Saito K., Yoshizaki T., Yui T., Yuzawa Y., Yoshida K.,      |             |     |        |
| RA     | Suzuki H., Taniuchi K., Wang K., Weller J., Whitaker G., Williams L., |             |     |        |
| RA     | Wynshaw-Boris A., Yoshida K., Hayakawa Y., Kawaji H., Kohno S.,       |             |     |        |
| RA     | Yuzawa Y.,  |             |     |        |
| RT     | Functional annotation of a full length mouse cDNA collection."        |             |     |        |
| RL     | Nature 409:685-690(2001).   |             |     |        |
| RN     | 121   |             |     |        |
| RF     | SEQUENCE FROM N.A.  |             |     |        |



DB 368 KEVL 372

RESULT 4

Query Match 12.7% Score 210 108.5 Length 106

Host Local Similarity 27.6% Pred. No. 20-100

Matches 40 Conservative 382 Mismatches 1027 Indels 592 Gaps 143

DB 272 AVEH:AVAN:GROVET:PEPE:292

DB 277 TAILMMW:MOJO:KRT:ITD:110:276

DB 223 PAAAVP:-----ALCAV:-----LCHROLD:RPAEA:FAAN:BERAL:LOH:CAR:BERHY:VAALD 271

DB 235 T3:SVH:HA:KAW:TAI:AS:PE:IT:110:276

DB 272 AVEH:AVAN:GROVET:PEPE:292

DB 277 TAILMMW:MOJO:KRT:ITD:110:276

DB 223 PAAAVP:-----ALCAV:-----LCHROLD:RPAEA:FAAN:BERAL:LOH:CAR:BERHY:VAALD 271

DB 235 T3:SVH:HA:KAW:TAI:AS:PE:IT:110:276

DB 272 AVEH:AVAN:GROVET:PEPE:292

DB 277 TAILMMW:MOJO:KRT:ITD:110:276

DB 223 PAAAVP:-----ALCAV:-----LCHROLD:RPAEA:FAAN:BERAL:LOH:CAR:BERHY:VAALD 271

DB 235 T3:SVH:HA:KAW:TAI:AS:PE:IT:110:276

DB 272 AVEH:AVAN:GROVET:PEPE:292

DB 277 TAILMMW:MOJO:KRT:ITD:110:276

DB 223 PAAAVP:-----ALCAV:-----LCHROLD:RPAEA:FAAN:BERAL:LOH:CAR:BERHY:VAALD 271

DB 235 T3:SVH:HA:KAW:TAI:AS:PE:IT:110:276

DB 272 AVEH:AVAN:GROVET:PEPE:292

DB 277 TAILMMW:MOJO:KRT:ITD:110:276

DB 223 PAAAVP:-----ALCAV:-----LCHROLD:RPAEA:FAAN:BERAL:LOH:CAR:BERHY:VAALD 271

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DB 235 T3:SVH:HA:KAW:TAI:AS:PE:IT:110:276

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DB 277 TAILMMW:MOJO:KRT:ITD:110:276

DB 223 PAAAVP:-----ALCAV:-----LCHROLD:RPAEA:FAAN:BERAL:LOH:CAR:BERHY:VAALD 271

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DB 277 TAILMMW:MOJO:KRT:ITD:110:276

DB 223 PAAAVP:-----ALCAV:-----LCHROLD:RPAEA:FAAN:BERAL:LOH:CAR:BERHY:VAALD 271

DB 235 T3:SVH:HA:KAW:TAI:AS:PE:IT:110:276

RN 111

RP SEQUENCE FROM N.A.

RC STRAIN:BERKELEY

RX MERRINE 20196006; JEMB-M-10721132

RA Adams M.D., Calinik S.E., Holt R.A., Evans G.A., Grayson J.D.,

RA Amaralides P.O., Schorl S.E., Li P.W., Hoskins R.A., Ballo R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Motman J.R., Yandell M.D., Zhang M., Chen L.X.,

RA Brandon R.C., Rogers Y.H.C., Blazer R.G., Champe M., Pottier R.D.,

RA Wan K.H., Doyle C., Baxter E.D., Heit G., Nelson C.R., Miklos G.L.D.,

RA Abrell J.F., Ashburner M., Au H., Andrews P., Balaban D.,

RA Ballo R.F., Past A., Pavlatidis J., Pavlatidis J., Pavlatidis J.,

RA Brown K.Y., Brown K.Y., Brown K.Y., Brown K.Y., Brown K.Y.,

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RA Brown K.Y., Brown K.Y., Brown K.Y., Brown K.Y., Brown K.Y.,

RA Brown K.Y., Brown K.Y., Brown K.Y., Brown K.Y., Brown K.Y.,

RESULT 6  
ID 014612 PRELIMINARY: PRT: 152 AA.  
DE 01 JAN 1998 (TREMBOLO, 05, Created)  
DE 01 JAN 1998 (TREMBOLO, 05, Last sequence update)  
DE 01 JUN 2001 (TREMBOLO, 17, Last annotation update)  
DE HYPOTHEtical, 17.8 KDa protein.  
OS Homo sapiens (human).  
OC Pkariotae; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
OX NCBI TaxID 9606;  
RN 111  
RD SEQUENCE FROM N.A.  
KA MEDLINE 97/97562; PubMed 9254601;  
KA Goto S., Akazawa S.K., Munkitaka P., Ichimori S.E., Chakraborty J.S.,  
Kobayashi J.M., Koster M., Kim Y.S., Emmert Buck M.R., Eickholt L.A.,  
Spiegel A.M., Bonner M., Roe B.A., Collins P.S., Burns A.L.,  
Marr C.L., Chaudhry-Barak O.,  
ET 7A. Genomic map for the 2.8 Mb region containing the multiple  
ET enhancer in the alpha 1 locus.  
DE Genomic Res. 7:729-735 (1997).  
DE EMBL: AF001439; AAC01205.1;  
DE JuncPro: J19001683; PX: 1;  
DE JuncPro: J1900787; PX: 1;  
DE SMART: SM00812; PX: 1;  
KW Hypothetical protein.  
SQ SEQUENCE 152 AA: 17764 MW: 2834667677386P GCGG4;  
  
Query Match 7.4% Score 122; DR 4; Length 152;  
Best local similarity 27.5% Prod. No. 0.0541;  
Matches 49; Conservative 24; Mismatches 61; Indels 18; Gaps 4;  
  
QY 78 FETASAKITPEKVSFVVYVGIIVIGTSPNNKAVLEPVSNAFISAFALPPEPEED 147  
DE 13 YVSDPRTKPKYTYEYKTAQFISKRPEDIKREVWVWVSRKRLGADLYRNLPR 72  
DE 138 VE-----FPEKHTEPFAEMTECEPRRALQEVYGLVAFVVERSEEDPTTRDELKAP 194  
DE 73 LTFEATPACVYCFPLASVTEREKADLRFTVITAFMS LGKRTT 124  
DE 194 GGLKAGVTRALEL--LRVLP 213  
DE 124 ---KGEVTRPVSRSRLDILP 142  
DE 111  
RD SEQUENCE FROM N.A.  
KA MEDLINE 97/97562; PubMed 9254601;  
KA Goto S., Akazawa S.K., Munkitaka P., Ichimori S.E., Chakraborty J.S.,  
Kobayashi J.M., Koster M., Kim Y.S., Emmert Buck M.R., Eickholt L.A.,  
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DE JuncPro: J19001683; PX: 1;  
DE JuncPro: J1900787; PX: 1;  
DE SMART: SM00812; PX: 1;  
KW Hypothetical protein.  
SQ SEQUENCE 152 AA: 17764 MW: 2834667677386P GCGG4;  
  
Query Match 7.4% Score 122; DR 11; Length 447;  
Best local similarity 27.5% Prod. No. 0.011;  
Matches 49; Conservative 24; Mismatches 61; Indels 18; Gaps 4;

Matches 39; Conservative 24; Mismatches 61; Indels 18; Gaps 4;  
  
QY 78 FETASAKITPEKVSFVVYVGIIVIGTSPNNKAVLEPVSNAFISAFALPPEPEED 147  
DE 13 YVSDPRTKPKYTYEYKTAQFISKRPEDIKREVWVWVSRKRLGADLYRNLPR 72  
DE 138 VE-----FPEKHTEPFAEMTECEPRRALQEVYGLVAFVVERSEEDPTTRDELKAP 194  
DE 73 LTFEATPACVYCFPLASVTEREKADLRFTVITAFMS LGKRTT 124  
DE 194 GGLKAGVTRALEL--LRVLP 213  
DE 124 ---KGEVTRPVSRSRLDILP 142  
DE 111  
RD SEQUENCE FROM N.A.  
KA MEDLINE 97/97562; PubMed 9254601;  
KA Goto S., Akazawa S.K., Munkitaka P., Ichimori S.E., Chakraborty J.S.,  
Kobayashi J.M., Koster M., Kim Y.S., Emmert Buck M.R., Eickholt L.A.,  
Spiegel A.M., Bonner M., Roe B.A., Collins P.S., Burns A.L.,  
Marr C.L., Chaudhry-Barak O.,  
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DE Genomic Res. 7:729-735 (1997).  
DE EMBL: AF001439; AAC01205.1;  
DE JuncPro: J19001683; PX: 1;  
DE JuncPro: J1900787; PX: 1;  
DE SMART: SM00812; PX: 1;  
KW Hypothetical protein.  
SQ SEQUENCE 152 AA: 17764 MW: 2834667677386P GCGG4;  
  
Query Match 7.4% Score 118; DR 4; Length 169;  
Best local similarity 32.3% Prod. No. 0.01;  
Matches 49; Conservative 22; Mismatches 49; Indels 27; Gaps 7;  
  
QY 80 LASAPTEERKYSK--PVVGVIVIGTSPNNKAVLEPVSNAFISAFALPPEPEED 138  
DE 13 YVSDPRTKPKYTYEYKTAQFISKRPEDIKREVWVWVSRKRLGADLYRNLPR 72  
DE 138 VE-----FPEKHTEPFAEMTECEPRRALQEVYGLVAFVVERSEEDPTTRDELKAP 194  
DE 73 LTFEATPACVYCFPLASVTEREKADLRFTVITAFMS LGKRTT 124  
DE 194 GGLKAGVTRALEL--LRVLP 213  
DE 124 ---KGEVTRPVSRSRLDILP 142  
DE 111  
RD SEQUENCE FROM N.A.  
KA MEDLINE 97/97562; PubMed 9254601;  
KA Goto S., Akazawa S.K., Munkitaka P., Ichimori S.E., Chakraborty J.S.,  
Kobayashi J.M., Koster M., Kim Y.S., Emmert Buck M.R., Eickholt L.A.,  
Spiegel A.M., Bonner M., Roe B.A., Collins P.S., Burns A.L.,  
Marr C.L., Chaudhry-Barak O.,  
ET 7A. Genomic map for the 2.8 Mb region containing the multiple  
ET enhancer in the alpha 1 locus.  
DE Genomic Res. 7:729-735 (1997).  
DE EMBL: AF001439; AAC01205.1;  
DE JuncPro: J19001683; PX: 1;  
DE JuncPro: J1900787; PX: 1;  
DE SMART: SM00812; PX: 1;  
KW Hypothetical protein.  
SQ SEQUENCE 169 AA: 19818 MW: 651839644934P5D CCGG4;  
  
Query Match 7.4% Score 118; DR 4; Length 169;  
Best local similarity 32.3% Prod. No. 0.01;  
Matches 49; Conservative 22; Mismatches 49; Indels 27; Gaps 7;  
  
QY 80 LASAPTEERKYSK--PVVGVIVIGTSPNNKAVLEPVSNAFISAFALPPEPEED 138  
DE 13 YVSDPRTKPKYTYEYKTAQFISKRPEDIKREVWVWVSRKRLGADLYRNLPR 72  
DE 138 VE-----FPEKHTEPFAEMTECEPRRALQEVYGLVAFVVERSEEDPTTRDELKAP 194  
DE 73 LTFEATPACVYCFPLASVTEREKADLRFTVITAFMS LGKRTT 124  
DE 194 GGLKAGVTRALEL--LRVLP 213  
DE 124 ---KGEVTRPVSRSRLDILP 142  
DE 111  
RD SEQUENCE FROM N.A.  
KA MEDLINE 97/97562; PubMed 9254601;  
KA Goto S., Akazawa S.K., Munkitaka P., Ichimori S.E., Chakraborty J.S.,  
Kobayashi J.M., Koster M., Kim Y.S., Emmert Buck M.R., Eickholt L.A.,  
Spiegel A.M., Bonner M., Roe B.A., Collins P.S., Burns A.L.,  
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DE EMBL: AF001439; AAC01205.1;  
DE JuncPro: J19001683; PX: 1;  
DE JuncPro: J1900787; PX: 1;  
DE SMART: SM00812; PX: 1;  
KW Hypothetical protein.  
SQ SEQUENCE 169 AA: 19818 MW: 651839644934P5D CCGG4;  
  
Query Match 7.4% Score 122; DR 11; Length 447;  
Best local similarity 27.5% Prod. No. 0.011;  
Matches 49; Conservative 24; Mismatches 61; Indels 18; Gaps 4;





$$\begin{array}{l} \text{---} \text{X} \\ \text{---} \text{N} \end{array} \quad \begin{array}{l} \text{N}^{\oplus} \text{H}^{\oplus} \text{---} \text{FALID} \\ \text{---} \text{---} \end{array}$$















[illegible]

|     |   |                 |
|-----|---|-----------------|
| 10  | 08 DEC 2000   | 2000US-0251990. |
| 11  | 11 DEC 2000   | 2000US-0254097. |
| 12  | 05 JAN 2001   | 2001US-0259378. |
| XX  |   |                 |
| 1A  | (HUMAN ) HUMAN GENOME SCI INC.  |                 |
| XX  |   |                 |
| 11  | Rosen CA, Barash SC, Kohn SM.   |                 |
| XX  |   |                 |
| 108 | W11: 2001 48426/52.   |                 |
| 08  | N P508: AAK57171.   |                 |
| 11  | Notes as to collected human genome/Pharmaceutical and other polypeptides,     |                 |
| 17  | secreted and processed, diagnosing and/or treating cancers and                |                 |
| 17  | metastasis.   |                 |
| XX  |   |                 |
| 13  | claim 11, SEQ ID No 11983: 4071pp + Sequence Listing English.                 |                 |
| XX  |   |                 |
| 00  | AAK54702 to AAK54703 encodes the human immune/Pharmaceutical antigen (1)      |                 |
| 00  | antigenic determinants given in AAK54719 to AAK57192; (1) have cytostatic     |                 |
| 00  | activity, and can be used in gene therapy and vaccine production; (1)         |                 |
| 00  | proteins and polypeptides may be used in the present invention, diagnosis and |                 |
| 00  | treatment of diseases associated with inappropriate (1) expression, for       |                 |
| 00  | example, they may be used to treat disorders associated with decreased        |                 |
| 00  | expression by restoring mutations or deletions in a patient's genome          |                 |
| 00  | or affect the activity of (1) by expressing recombinant proteins or to        |                 |
| 00  | suppress the patient's own production of (1); Additionally, (1)               |                 |
| 00  | polypeptides may be used to produce the secreted (1); by inserting            |                 |
| 00  | the nucleotide into a host cell and culturing the cell to express the         |                 |
| 00  | protein; (1) proteins and polypeptides may be used to prevent,                |                 |
| 00  | diagnose and treat immune/Pharmaceutical-related diseases, especially         |                 |
| 00  | cancers and cancer metastases of hematopoietic derived cells; AAK54703        |                 |
| 00  | to AAK57192 represents a human immune/Pharmaceutical antigen sequence         |                 |
| 00  | sequence from the present invention; AAK57192 to AAK57196 and AAK57199        |                 |
| XX  | represent sequences used in the compilation of the present invention.         |                 |
| 50  | Sequence: 93 AA:  |                 |
| 00  |   |                 |
| 00  | Query Match 15.18; Score 249; 148 227 Length 942                              |                 |
| 00  | Best Local Similarity 100.0%; Ident. No. 50 18;                               |                 |
| 00  | Matches: 49, Coverage: 66.6; Mismatches: 0; Indels: 0; Gaps: 0;               |                 |
| 00  |   |                 |
| 00  | 1 MASTFHDSHGCMHTLLGCTAKIGCFARVATGTHHGHGSHSL 43                                |                 |
| 00  |   |                 |
| 00  | 46 MASPHDSHGCMHTLLGCTAKIGCFARVATGTHHGHGSHSL 88                                |                 |
| 00  |   |                 |
| 00  | RESULT 7  |                 |
| 00  | AAK59625  |                 |
| 11  | AAK59625 standard; protein: 295 AA.   |                 |
| XX  |   |                 |
| 00  | 26 MAR 2002 (first entry)   |                 |
| XX  |   |                 |
| 100 | Inosophthal melanostar polypeptide SEQ ID No 5667.                            |                 |
| XX  |   |                 |
| 00  | Pharmaceutical; developmental biology; cell signaling; insecticide;           |                 |
| 00  | Pharmaceutical.   |                 |
| XX  |   |                 |
| 00  | Inosophthal melanostar.   |                 |
| XX  |   |                 |
| 108 | W0200171042 A2.   |                 |
| XX  |   |                 |
| 00  | 27-SEP 2001.  |                 |
| XX  |   |                 |
| 00  | 23 MAR 2001: 2001WO-0509231.  |                 |
| XX  |   |                 |
| 108 | 23 MAR 2000: 2000US-191637P.  |                 |
| 108 | 11-JUL-2000: 2000US-0614150.  |                 |
| XX  |   |                 |
| 1A  | (PEKE ) PE OAKP NY.   |                 |
| XX  |   |                 |







































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